

SEQUENCE LISTING

<110> Yumin, Tao
 Gordon-Kamm, William
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 Lowe, Keith
 Danilevskaya, Olga
 Mahajan, Pramod
 Rafalski, Jan Antoni
 Sakai, Hajime
 Klein, Theodore

<120> Transcriptional Regulatory Nucleic
 Acids, Polypeptides, and Methods of Use Thereof

<130> 1288R

<150> 10/005,057

<151> 2001-12-04

<150> 60/251,555

<151> 2000-12-06

<160> 43

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<212> DNA

<213> Zea mays

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Glu Arg Leu Leu Asp Arg Asp Gln Val Asp Gly Asp Glu Ser Val Glu	
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 gat gaa gaa gaa gat gga ttc tta aaa gga ttc aag gtt gca aac ttt	143
Asp Glu Glu Glu Asp Gly Phe Leu Lys Gly Phe Lys Val Ala Asn Phe	
35 40 45	
 gaa tat atc gat gag gca aag gct cag gca gaa aaa gag gag gca cgg	191
Glu Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg	
50 55 60	

aga aag gct gca gct gag gct gaa aat tct gaa aga aac tac tgg gat Arg Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp 65 70 75	239
gaa cta ttg aag gat aga tat gat gta cag aaa gtt gaa gaa cat act Glu Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr 80 85 90 95	287
gct atg gga aaa ggg aaa aga agc cgc aaa cag atg gct gcc gct gat Ala Met Gly Lys Gly Lys Arg Ser Arg Lys Gln Met Ala Ala Ala Asp 100 105 110	335
gaa gat gac att cat gat tta agt tcc gaa gat gag gat tac tca ttg Glu Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu 115 120 125	383
gag gat gac att tca gat aat gac aca agt ttg caa gga aat att tct Glu Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser 130 135 140	431
ggg aag agg gga caa tat tct aag aga aaa tca cgt aat gtt gat tct Gly Lys Arg Gly Gln Tyr Ser Lys Arg Lys Ser Arg Asn Val Asp Ser 145 150 155	479
att cca ttg atg gag ggc gaa gga cgt acc ttg aga gtt ctt gga ttc Ile Pro Leu Met Glu Gly Glu Gly Arg Thr Leu Arg Val Leu Gly Phe 160 165 170 175	527
aac cat gct caa cga gca atg ttc cta cag aca ctc aat aga ttc ggt Asn His Ala Gln Arg Ala Met Phe Leu Gln Thr Leu Asn Arg Phe Gly 180 185 190	575
ttt cag aat tat gac tgg aaa gag tat ctt cct cgt ctt aaa gga aaa Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys Gly Lys 195 200 205	623
agt gtc gag gaa atc cag aga tat gct gaa ctt gtc atg gca cat ctt Ser Val Glu Glu Ile Gln Arg Tyr Ala Glu Leu Val Met Ala His Leu 210 215 220	671
gtt gaa gaa att aat gat tct gac tat ttt tca gat ggc gtt cca aag Val Glu Glu Ile Asn Asp Ser Asp Tyr Phe Ser Asp Gly Val Pro Lys 225 230 235	719
gaa atg atg cgt gtt gat gat gta cta gtc agg ata gca aac ata tcc Glu Met Met Arg Val Asp Asp Val Leu Val Arg Ile Ala Asn Ile Ser 240 245 250 255	767
ctt atc gag gag aag atg gct gcc aca gga cca gga aaa att aca aac Leu Ile Glu Glu Lys Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn 260 265 270	815
att ttt cct aat tac ttg ctc tat gag ttc caa ggc tta tct ggt gga Ile Phe Pro Asn Tyr Leu Leu Tyr Glu Phe Gln Gly Leu Ser Gly Gly 275 280 285	863

aga ata tgg aaa gcg gag cat gat cta ctg tta ctg aga ggc ata ctg Arg Ile Trp Lys Ala Glu His Asp Leu Leu Leu Leu Arg Gly Ile Leu 290 295 300	911
aag cat gga tat gca agg tgg cag tat ata tca gat gac aga gag aat Lys His Gly Tyr Ala Arg Trp Gln Tyr Ile Ser Asp Asp Arg Glu Asn 305 310 315	959
ggg ctt ttt gag gct gca cga cga gag ctg cat ctc cct tcg gtt aat Gly Leu Phe Glu Ala Ala Arg Arg Glu Leu His Leu Pro Ser Val Asn 320 325 330 335	1007
gaa ata att ggt gct cag ttg aac gag gca aat ggg aat ttg gaa ggt Glu Ile Ile Gly Ala Gln Leu Asn Glu Ala Asn Gly Asn Leu Glu Gly 340 345 350	1055
gca cag gaa ggc caa gcg aac aca aca agc atg tcg cat tac aag gag Ala Gln Glu Gly Gln Ala Asn Thr Thr Ser Met Ser His Tyr Lys Glu 355 360 365	1103
atc cag aga aag ata gtt gag ttc ttg aga aag aga tat cat ctt atg Ile Gln Arg Lys Ile Val Glu Phe Leu Arg Lys Arg Tyr His Leu Met 370 375 380	1151
gag aga gcc ttg aat ctg gaa tat gct gtg ata aag aaa aaa att cct Glu Arg Ala Leu Asn Leu Glu Tyr Ala Val Ile Lys Lys Lys Ile Pro 385 390 395	1199
gtt cct gat gat att act gaa caa ggt gtt cca gca gga cat gct ccg Val Pro Asp Asp Ile Thr Glu Gln Gly Val Pro Ala Gly His Ala Pro 400 405 410 415	1247
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cca att tct acc aat gaa ttg att tct gag ggc aca gct ggt cag tta Pro Ile Ser Thr Asn Glu Leu Ile Ser Glu Gly Thr Ala Gly Gln Leu 435 440 445	1343
caa gtt ccc cat ctc tac aat aag atg tgt gga gtg ctt gaa gag agt Gln Val Pro His Leu Tyr Asn Lys Met Cys Gly Val Leu Glu Glu Ser 450 455 460	1391
ggt gct tat gcg ctc agt tcc ttc ttt gga gac aag tcc gca tct tct Gly Ala Tyr Ala Leu Ser Ser Phe Phe Gly Asp Lys Ser Ala Ser Ser 465 470 475	1439
act ttg gcc aat agc ctt cga cag ttt gaa act gtg tgt gag aat gtc Thr Leu Ala Asn Ser Leu Arg Gln Phe Glu Thr Val Cys Glu Asn Val 480 485 490 495	1487
gtc gag gcc tta cga cca cac caa aat ggt act gcc agt gcc atc aaa Val Glu Ala Leu Arg Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys 500 505 510	1535

gag gaa ttg gta gat gca gcc acc aaa gca gca gca gca gca gct cct 1583
 Glu Glu Leu Val Asp Ala Ala Thr Lys Ala Ala Ala Ala Ala Ala Pro
 515 520 525

caa caa gat tca ggc cat gat gca ccg cat ggg cag tct tcg aca gcc 1631
 Gln Gln Asp Ser Gly His Asp Ala Pro His Gly Gln Ser Ser Thr Ala
 530 535 540

aag gcg gac atg gaa atc gat ggt tgattttgtag gttccagagt ggcaagaaag 1685
 Lys Ala Asp Met Glu Ile Asp Gly
 545 550

ggaatcccct ctaatcatta tgtatactgt ggtcagaatg tccgctatat attgtaacat 1745
 caaagaaagc acctccaggc ctgaggggtgt tactgctaata gcgtttgggt tactttgtcct 1805
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 aaaaaaaaaa 1874

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 <213> Zea mays

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 35 40 45
 Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg Arg
 50 55 60
 Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp Glu
 65 70 75 80
 Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr Ala
 85 90 95
 Met Gly Lys Gly Lys Arg Ser Arg Lys Gln Met Ala Ala Ala Asp Glu
 100 105 110
 Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu Glu
 115 120 125
 Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser Gly
 130 135 140
 Lys Arg Gly Gln Tyr Ser Lys Arg Lys Ser Arg Asn Val Asp Ser Ile
 145 150 155 160
 Pro Leu Met Glu Gly Glu Gly Arg Thr Leu Arg Val Leu Gly Phe Asn
 165 170 175
 His Ala Gln Arg Ala Met Phe Leu Gln Thr Leu Asn Arg Phe Gly Phe
 180 185 190
 Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys Gly Lys Ser
 195 200 205
 Val Glu Glu Ile Gln Arg Tyr Ala Glu Leu Val Met Ala His Leu Val
 210 215 220
 Glu Glu Ile Asn Asp Ser Asp Tyr Phe Ser Asp Gly Val Pro Lys Glu
 225 230 235 240
 Met Met Arg Val Asp Asp Val Leu Val Arg Ile Ala Asn Ile Ser Leu
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 Ile Glu Glu Lys Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn Ile

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23

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Arg Arg Leu Arg Ala Glu Gly His Arg Val Leu Leu Phe Ala Gln Met
5 10 15

act aaa atg ttg gac att ctt gag gat tac atg aat ttc aga aaa ttc 152
Thr Lys Met Leu Asp Ile Leu Glu Asp Tyr Met Asn Phe Arg Lys Phe
20 25 30 35

aag tat ttc aga ctt gat ggg tct tca gcc atc tca gac cgc cgt gac 200
Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp Arg Arg Asp
40 45 50

atg gtc cga gat ttt cag aac agg aat gac ata ttt gtt ttc ttg tta 248
Met Val Arg Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu
55 60 65

agc aca aga gct ggg ggg ctt ggt att aat ttg act gct gct gat act 296
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Ala Asp Thr
70 75 80

gtt att ttt tat gaa att gac tgg aat cca aca caa gac cag cag gca 344
Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp Gln Gln Ala
85 90 95

atg gat aga aca cac aga ctt ggt caa aca aag gag gta act gtg tac 392
Met Asp Arg Thr His Arg Leu Gly Gln Thr Lys Glu Val Thr Val Tyr
100 105 110 115

agg ctt ata tgc aaa gat acc att gag gag aaa ata ttg caa aga gca 440
Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu Gln Arg Ala
120 125 130

aag cag aaa aat gca gtg caa gag tta gtt atg aag ggg aaa cat gtc 488
Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly Lys His Val
135 140 145

caa gac gat cat ttg atg aga caa gag gat gtt gtt tca tta ctt att	536
Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser Leu Leu Ile	
150 155 160	
gat gac aca cag att gca cac aag ttg aaa gaa ata tcc atg cag gcg	584
Asp Asp Thr Gln Ile Ala His Lys Leu Lys Glu Ile Ser Met Gln Ala	
165 170 175	
aag gat cga caa aag agg aga cga gcg aag ggc atc aag gtt gac aaa	632
Lys Asp Arg Gln Lys Arg Arg Arg Ala Lys Gly Ile Lys Val Asp Lys	
180 185 190 195	
gaa gga gat ttg acg ctc gaa gac ttg gat gat gct act gca gaa gct	680
Glu Gly Asp Leu Thr Leu Glu Asp Leu Asp Asp Ala Thr Ala Glu Ala	
200 205 210	
gta gat caa gac aaa acg acc agc aaa aag aaa aag agc tcc cac aag	728
Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Ser Ser His Lys	
215 220 225	
aaa cat acg aat act cat gat aat gac aat ata gac aag aat gga gag	776
Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys Asn Gly Glu	
230 235 240	
gcc gat gtg gga gat cat ccg ggg agt agt aac aca gaa aac gaa cag	824
Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu Asn Glu Gln	
245 250 255	
atg ccc gaa tca aga cct aaa aga tca aaa agg ctg atg aag agc att	872
Met Pro Glu Ser Arg Pro Lys Arg Ser Lys Arg Leu Met Lys Ser Ile	
260 265 270 275	
act gat gac aag gaa cta gct gct gct gcg gat cat gag aaa ccg gta	920
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<212> PRT

<213> Zea mays

<220>

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			20					25					30		

Arg Lys Phe Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp
 35 40 45
 Arg Arg Asp Met Val Arg Asp Phe Gln Asn Arg Asn Asp Ile Phe Val
 50 55 60
 Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala
 65 70 75 80
 Ala Asp Thr Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp
 85 90 95
 Gln Gln Ala Met Asp Arg Thr His Arg Leu Gly Gln Thr Lys Glu Val
 100 105 110
 Thr Val Tyr Arg Leu Ile Cys Lys Asp Thr Ile Glu Glu Lys Ile Leu
 115 120 125
 Gln Arg Ala Lys Gln Lys Asn Ala Val Gln Glu Leu Val Met Lys Gly
 130 135 140
 Lys His Val Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser
 145 150 155 160
 Leu Leu Ile Asp Asp Thr Gln Ile Ala His Lys Leu Lys Glu Ile Ser
 165 170 175
 Met Gln Ala Lys Asp Arg Gln Lys Arg Arg Arg Ala Lys Gly Ile Lys
 180 185 190
 Val Asp Lys Glu Gly Asp Leu Thr Leu Glu Asp Leu Asp Asp Ala Thr
 195 200 205
 Ala Glu Ala Val Asp Gln Asp Lys Thr Thr Ser Lys Lys Lys Lys Ser
 210 215 220
 Ser His Lys Lys His Thr Asn Thr His Asp Asn Asp Asn Ile Asp Lys
 225 230 235 240
 Asn Gly Glu Ala Asp Val Gly Asp His Pro Gly Ser Ser Asn Thr Glu
 245 250 255
 Asn Glu Gln Met Pro Glu Ser Arg Pro Lys Arg Ser Lys Arg Leu Met
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gaa ttc aaa acc tgg gct ccc agt att ggg aca att ctg tat gat ggt 95
Glu Phe Lys Thr Trp Ala Pro Ser Ile Gly Thr Ile Leu Tyr Asp Gly
20 25 30

cgt cca gaa gag agg aag ctt tta agg gaa aag aat ttt gat gga ttg 143
Arg Pro Glu Glu Arg Lys Leu Leu Arg Glu Lys Asn Phe Asp Gly Leu
35 40 45

caa ttt aat gtt ttg ctc acg cat tat gac ttg ata ctg aaa gat aag 191
Gln Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys
50 55 60

aag ttc cta aag aaa gtt cac tgg cat tat ttg att gtt gat gaa gga 239
Lys Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly
65 70 75

cat cgt ctg aaa aat cat gaa tgt gct ctt gct cgc aca cta gtt tca 287
His Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser
80 85 90 95

gga tat cag atc cgc cgc aga cta ctt tta act ggc act cca atc caa 335
Gly Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln
100 105 110

aat agc cta caa gaa ctg tgg tct ttg ctt aac ttt att ctg ccc aat 383
Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn
115 120 125

att ttt aat tca tct cag aat ttt gag gaa tgg ttt aat gca cca ttt 431
Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe
130 135 140

gca tgt gat gtt agt ctt aat gat gag gaa cag cta tta atc ata cat 479
Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His
145 150 155

cgt ctg cat caa gtt ttg cgt cca ttt ttg ctg agg agg aaa aaa gat 527
Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp
160 165 170 175

gaa gtg gaa aaa tat ctc cct gtc aaa aca caa gta att ctc aag tgt	575
Glu Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys	
180 185 190	
gat atg tct gct tgg caa aaa gca tac tat gaa caa gtc aca agc agg	623
Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg	
195 200 205	
gaa aag gtt gca cta gga ttt ggg ctc aga tca aag gct ctg cag aat	671
Glu Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn	
210 215 220	
ctg tca atg caa ctt agg aaa tgt tgc aac cac ccc tat cta ttt gta	719
Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val	
225 230 235	
gag cac tac aac atg tac cag cgg gag gaa att gtt aga gca tca ggg	767
Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly	
240 245 250 255	
aag ttt gaa ttg ctt gat cgt cta ctt cca aaa ctg cag aga gct ggt	815
Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly	
260 265 270	
cac agg gtt ctg ctt ttc tct cag atg acg aaa ctg ctt gat gtt tta	863
His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu	
275 280 285	
gaa ata tat ttg caa atg tac aat ttc aag tac atg agg ctt gat gga	911
Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly	
290 295 300	
tcc acg aag act gaa gaa cga ggg agg tta ctg gca gat ttt aat aag	959
Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys	
305 310 315	
aag gat tcg gaa tat ttc atg ttt ctc ctc agc aca cgt gct gga gga	1007
Lys Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly	
320 325 330 335	
ctt ggg ttg aac ttg cag acg gcg gac act gtc att ata ttt gat agt	1055
Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser	
340 345 350	
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Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg	
355 360 365	
ata ggc aga aga atg aag tgc gtg tgt ttg ttc ttg tta gtg tcg gct	1151
Ile Gly Arg Arg Met Lys Cys Val Cys Leu Phe Leu Leu Val Ser Ala	
370 375 380	
cca ttg aag aag aga tcc tgg acc gtg caa aac aaa aga tgg gta tcg	1199
Pro Leu Lys Lys Arg Ser Trp Thr Val Gln Asn Lys Arg Trp Val Ser	
385 390 395	

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Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg Arg Gly Thr Ser	
420 425 430	
tcg ctg gga aca gat atc ccc agt gag cgc gag ata aat cgt ttg gct	1343
Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile Asn Arg Leu Ala	
435 440 445	
gca cga act gat gaa gaa ttc tgg ttg ttt gag aag atg gat gaa gaa	1391
Ala Arg Thr Asp Glu Glu Phe Trp Leu Phe Glu Lys Met Asp Glu Glu	
450 455 460	
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Arg Arg Leu Arg Glu Asn Tyr Lys Ser Arg Leu Met Asp Gly Asn Glu	
465 470 475	
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Val Pro Asp Trp Val Phe Ala Asn Asn Asp Leu Pro Lys Arg Thr Val	
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gca gat gag ttc cag aat ata atg gtc ggt gcg aag cga cgt aga aag	1535
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500 505 510	
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Glu Val Val Tyr Ser Asp Ser Phe Gly Asp Gln Trp Met Lys Ser Asp	
515 520 525	
gag gga ttt gaa gac att cca aag gcg act cag agg tcg aag aag act	1631
Glu Gly Phe Glu Asp Ile Pro Lys Ala Thr Gln Arg Ser Lys Lys Thr	
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gct tac tca tct gac atc caa gtt gag ttt agt gaa agg agg aaa aga	1679
Ala Tyr Ser Ser Asp Ile Gln Val Glu Phe Ser Glu Arg Arg Lys Arg	
545 550 555	
cct agg tct gta gaa aac agc gca gac ggt gtg agc aac ccg acg tgg	1727
Pro Arg Ser Val Glu Asn Ser Ala Asp Gly Val Ser Asn Pro Thr Trp	
560 565 570 575	
acg cct gac aaa gga agg gct gga gtt tca tca tac agc aag gac gag	1775
Thr Pro Asp Lys Gly Arg Ala Gly Val Ser Ser Tyr Ser Lys Asp Glu	
580 585 590	
act gaa gat gat ggc gaa gac gaa gtc att act agc ggc tta caa aag	1823
Thr Glu Asp Asp Gly Glu Asp Glu Val Ile Thr Ser Gly Leu Gln Lys	
595 600 605	
gga aac agt ttc aca tgg aat acc cta gga aga aga agg tca agc cac	1871
Gly Asn Ser Phe Thr Trp Asn Thr Leu Gly Arg Arg Arg Ser Ser His	
610 615 620	

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625 630 635

1913

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<212> PRT
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35 40 45
Phe Asn Val Leu Leu Thr His Tyr Asp Leu Ile Leu Lys Asp Lys Lys
50 55 60
Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly His
65 70 75 80
Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser Gly
85 90 95
Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn
100 105 110
Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn Ile
115 120 125
Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe Ala
130 135 140
Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His Arg
145 150 155 160
Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp Glu
165 170 175
Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys Asp
180 185 190
Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg Glu
195 200 205
Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn Leu
210 215 220
Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val Glu
225 230 235 240
His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly Lys
245 250 255
Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly His
260 265 270
Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu Glu
275 280 285
Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly Ser
290 295 300
Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys Lys
305 310 315 320
Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu
325 330 335
Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser Asp
340 345 350

Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp Arg Ala His Arg Ile
 355 360 365
 Gly Arg Arg Met Lys Cys Val Cys Leu Phe Leu Leu Val Ser Ala Pro
 370 375 380
 Leu Lys Lys Arg Ser Trp Thr Val Gln Asn Lys Arg Trp Val Ser Met
 385 390 395 400
 Gln Lys Leu Leu Gln Ala Gly Leu Phe Asn Thr Thr Ser Thr Ala Gln
 405 410 415
 Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg Arg Gly Thr Ser Ser
 420 425 430
 Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile Asn Arg Leu Ala Ala
 435 440 445
 Arg Thr Asp Glu Glu Phe Trp Leu Phe Glu Lys Met Asp Glu Glu Arg
 450 455 460
 Arg Leu Arg Glu Asn Tyr Lys Ser Arg Leu Met Asp Gly Asn Glu Val
 465 470 475 480
 Pro Asp Trp Val Phe Ala Asn Asn Asp Leu Pro Lys Arg Thr Val Ala
 485 490 495
 Asp Glu Phe Gln Asn Ile Met Val Gly Ala Lys Arg Arg Arg Lys Glu
 500 505 510
 Val Val Tyr Ser Asp Ser Phe Gly Asp Gln Trp Met Lys Ser Asp Glu
 515 520 525
 Gly Phe Glu Asp Ile Pro Lys Ala Thr Gln Arg Ser Lys Lys Thr Ala
 530 535 540
 Tyr Ser Ser Asp Ile Gln Val Glu Phe Ser Glu Arg Arg Lys Arg Pro
 545 550 555 560
 Arg Ser Val Glu Asn Ser Ala Asp Gly Val Ser Asn Pro Thr Trp Thr
 565 570 575
 Pro Asp Lys Gly Arg Ala Gly Val Ser Ser Tyr Ser Lys Asp Glu Thr
 580 585 590
 Glu Asp Asp Gly Glu Asp Glu Val Ile Thr Ser Gly Leu Gln Lys Gly
 595 600 605
 Asn Ser Phe Thr Trp Asn Thr Leu Gly Arg Arg Arg Ser Ser His Phe
 610 615 620
 Ser Ser Ser Ser Asp Ser Arg Gly Arg Pro Thr Phe
 625 630 635

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 11
 cgaattcaaa acctgggctc cca

23

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind

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<222> (1)...(21)

<400> 12
ttagaatgtt gggcgccctc t                                     21

<210> 13
<211> 1463
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)...(1460)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 13
gt cga ccc acg cgt ccg cca gaa gag cgg aac cat ata agg gac aat      47
  Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn
    1             5             10             15

ttg ctg caa cct ggg aaa ttt gat gtg tgt gtg act agt ttt gaa atg      95
Leu Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met
          20             25             30

gca atc aaa gaa aaa tct gcg ttg agg cgc ttc agc tgg cgc tac ata      143
Ala Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile
          35             40             45

atc att gat gaa gct cac cgg ata aaa aat gaa aat tct ctt cta tca      191
Ile Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser
          50             55             60

aag act atg agg att tac aac act aat tat cgt ctc ctc atc aca ggc      239
Lys Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Leu Ile Thr Gly
          65             70             75

act cca ctc cag aat aat ctc cat gag ctc tgg gct ctc ctc aat ttc      287
Thr Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe
          80             85             90             95

ttg cta cct gaa ata ttt agc tct gcg gag acc ttt gat gaa tgg ttt      335
Leu Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe
          100             105             110

caa ata tct ggg gaa aat gat caa cag gag gtg gtg cag cag ctt cat      383
Gln Ile Ser Gly Glu Asn Asp Gln Gln Glu Val Val Gln Gln Leu His
          115             120             125

aag gtt ctt cgc cca ttc ctt ctt agg agg ctc aag tct gat gta naa      431
Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Ser Asp Val Xaa
          130             135             140

aag ggc cta cct cca aag aaa gaa aca att ctt aaa gtt gga atg tct      479

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Lys	Gly	Leu	Pro	Pro	Lys	Lys	Glu	Thr	Ile	Leu	Lys	Val	Gly	Met	Ser	
145						150					155					
cag	atg	caa	aag	cag	tac	tat	cgt	gct	ctg	ctt	cag	aag	gat	ttg	gag	527
Gln	Met	Gln	Lys	Gln	Tyr	Tyr	Arg	Ala	Leu	Leu	Gln	Lys	Asp	Leu	Glu	
160					165					170					175	
ggt	att	aat	gct	ggt	ggt	gaa	cgc	aag	cga	ttg	ctt	aac	att	gcc	atg	575
Val	Ile	Asn	Ala	Gly	Gly	Glu	Arg	Lys	Arg	Leu	Leu	Asn	Ile	Ala	Met	
				180					185					190		
cag	ttg	cgc	aag	tgc	tgc	aac	cat	cca	tat	tta	ttc	caa	gga	gct	gaa	623
Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro	Tyr	Leu	Phe	Gln	Gly	Ala	Glu	
			195					200					205			
cct	ggg	cca	ccc	tac	aca	act	ggt	gaa	cat	cta	att	gag	aat	gca	gga	671
Pro	Gly	Pro	Pro	Tyr	Thr	Thr	Gly	Glu	His	Leu	Ile	Glu	Asn	Ala	Gly	
		210					215					220				
aaa	atg	gtt	cta	ctt	gat	aaa	ttg	ctg	ccc	aag	cta	aag	gag	cgt	gat	719
Lys	Met	Val	Leu	Leu	Asp	Lys	Leu	Leu	Pro	Lys	Leu	Lys	Glu	Arg	Asp	
	225					230					235					
tcc	aga	gtc	ctt	att	ttt	tca	cag	atg	acc	agg	ctt	ttg	gat	atc	ttg	767
Ser	Arg	Val	Leu	Ile	Phe	Ser	Gln	Met	Thr	Arg	Leu	Leu	Asp	Ile	Leu	
240					245					250					255	
gaa	gat	tat	ctt	atg	tat	agg	gga	tat	cag	tat	tgt	cga	att	gat	gga	815
Glu	Asp	Tyr	Leu	Met	Tyr	Arg	Gly	Tyr	Gln	Tyr	Cys	Arg	Ile	Asp	Gly	
				260					265					270		
aat	aca	ggt	gga	gaa	gat	cgt	gat	gca	tcc	att	gaa	gcc	ttc	aat	agt	863
Asn	Thr	Gly	Gly	Glu	Asp	Arg	Asp	Ala	Ser	Ile	Glu	Ala	Phe	Asn	Ser	
			275					280					285			
cca	gga	agt	gag	aag	ttt	gtt	ttc	tta	ctt	tca	act	agg	gca	ggt	ggc	911
Pro	Gly	Ser	Glu	Lys	Phe	Val	Phe	Leu	Leu	Ser	Thr	Arg	Ala	Gly	Gly	
		290					295					300				
ctt	ggt	atc	aac	ttg	gcc	act	gct	gat	gtt	gtg	gtt	ctc	tat	gac	agc	959
Leu	Gly	Ile	Asn	Leu	Ala	Thr	Ala	Asp	Val	Val	Val	Leu	Tyr	Asp	Ser	
	305					310					315					
gat	tgg	aat	ccc	caa	gct	gat	ctg	caa	gct	cag	gac	cgt	gca	cat	aga	1007
Asp	Trp	Asn	Pro	Gln	Ala	Asp	Leu	Gln	Ala	Gln	Asp	Arg	Ala	His	Arg	
320					325					330					335	
ata	ggt	caa	aaa	gaa	aga	agt	tca	agt	gtt	ccg	ctt	ttg	cac	ttg	agt	1055
Ile	Gly	Gln	Lys	Glu	Arg	Ser	Ser	Ser	Val	Pro	Leu	Leu	His	Leu	Ser	
				340					345					350		
tca	act	att	gag	gaa	aag	gtg	att	gag	aga	gca	tat	aag	aag	cta	gca	1103
Ser	Thr	Ile	Glu	Lys	Val	Ile	Glu	Arg	Ala	Tyr	Lys	Lys	Lys	Leu	Ala	
			355				360					365				
ttg	gat	gct	ttg	gtt	att	cag	caa	gga	cga	ttg	gca	gag	cag	aaa	act	1151

Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr	
370 375 380	
gtc aat aag gat gat ctt ctg caa atg gtg cgg ttt ggt gct gaa atg	1199
Val Asn Lys Asp Asp Leu Leu Gln Met Val Arg Phe Gly Ala Glu Met	
385 390 395	
gtt ttc agt tct aag gac agc aca ata act gat gag gac att gac cgt	1247
Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg	
400 405 410 415	
att ata gct aaa gga gag gag aca aca gca gaa ctt gat gcg aaa atg	1295
Ile Ile Ala Lys Gly Glu Glu Thr Thr Ala Glu Leu Asp Ala Lys Met	
420 425 430	
aaa aag ttc act gag gat gcc atc aaa ttt aag atg gat gat aat gct	1343
Lys Lys Phe Thr Glu Asp Ala Ile Lys Phe Lys Met Asp Asp Asn Ala	
435 440 445	
gaa ttg tat gac ttc gat gat gag aag gat gaa aac aag gtt gat ttc	1391
Glu Leu Tyr Asp Phe Asp Asp Glu Lys Asp Glu Asn Lys Val Asp Phe	
450 455 460	
aag aaa ctt gtt agt gat aac tgg att gag cca cct aga aga gaa agg	1439
Lys Lys Leu Val Ser Asp Asn Trp Ile Glu Pro Pro Arg Arg Glu Arg	
465 470 475	
aag nga aac tac tct gag tct tga	1463
Lys Xaa Asn Tyr Ser Glu Ser	
480 485	

<210> 14
 <211> 486
 <212> PRT
 <213> Zea mays

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

<400> 14

Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn Leu	
1 5 10 15	
Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met Ala	
20 25 30	
Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile	
35 40 45	
Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys	
50 55 60	
Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Ile Thr Gly Thr	
65 70 75 80	
Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu	
85 90 95	
Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln	


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<221> primer_bind
<222> (1)...(23)

<400> 15
ccagaagagc ggaaccatat aag                                     23

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 16
ctcttctagg tggctcaatc cag                                     23

<210> 17
<211> 1645
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (2)...(1642)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 17
a gca gat ggg aga aga tac atg atc cgc cgg aga cta ctt tta aca ggc      49
  Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly
    1             5             10             15

act cct atc caa aac agc ctg caa gag ctc tgg tct ttg ctt aac ttc      97
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe
    20             25             30

atc ctg ccc aat att ttt aat tca tcc cag aat ttt gag gaa tgg ttt      145
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe
    35             40             45

aat gca cca ttt gca tgt gat gtc agt ctt aat gat gag gaa caa cta      193
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu
    50             55             60

cta atc ata cat cgt ttg cat caa gtt ttg cgt cca ttc ttg ctg agg      241
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg
    65             70             75             80

agg aag aaa gat gaa gta nag aaa tat ctc cct gtg aaa aca caa gta      289
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val
    85             90             95

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att ctc aag tgt gac atg tct gct tgg caa aaa gca tac tac gaa caa Ile Leu Lys Cys Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln 100 105 110	337
gtc aca agc agg gaa aag gtt gcg cta gga tat ggg atc aga aag aag Val Thr Ser Arg Glu Lys Val Ala Leu Gly Tyr Gly Ile Arg Lys Lys 115 120 125	385
gct ctg caa aat ctg tca atg caa ctt agg aag tgt tgc aat cat ccc Ala Leu Gln Asn Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro 130 135 140	433
tac cta ttc gta gag cat tat aac atg tac caa cgg gag gaa ata gtt Tyr Leu Phe Val Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val 145 150 155 160	481
aga gca tcc gga aag ttt gaa ttg ctt gat cgt cta ctt ccg aaa ttg Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu 165 170 175	529
cag aga gct ggt cac agg gtt tta ctt ttc tct cag atg aca aaa ttg Gln Arg Ala Gly His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu 180 185 190	577
ctt gac gtt tta gaa ata tat ttg cag atg tac aat ttc aag tac atg Leu Asp Val Leu Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met 195 200 205	625
agg ctt gat gga tcc aca aag act gaa gaa cgt ggg agg tta ctg gca Arg Leu Asp Gly Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala 210 215 220	673
gat ttt aat aag aag aat tca gaa tat ttc atg ttt ctt ctc agc aca Asp Phe Asn Lys Lys Asn Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr 225 230 235 240	721
cga gcc gga ggt ctt gga ttg aac ttg cag act gca gac acc gtc att Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile 245 250 255	769
atc ttt gat agt gac tgg aac cct cag atg gac caa caa gct gag gac Ile Phe Asp Ser Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp 260 265 270	817
cgt gcc cat cgt ata ggg caa aag aac gaa gta cgt gtg ttt gtt ctt Arg Ala His Arg Ile Gly Gln Lys Asn Glu Val Arg Val Phe Val Leu 275 280 285	865
gtt agc gtt ggt tca att gaa gaa gag ata ttg gat cgt gcg aaa cag Val Ser Val Gly Ser Ile Glu Glu Glu Ile Leu Asp Arg Ala Lys Gln 290 295 300	913
aag atg ggt att gat gca aaa gta atc cag gct ggg ttg ttt aac acg Lys Met Gly Ile Asp Ala Lys Val Ile Gln Ala Gly Leu Phe Asn Thr 305 310 315 320	961

acc tcc aca gca cag gac agg cga gca ttg ctg cag gag ata ctc agg	1009
Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg	
325 330 335	
aga gga aca agc tca ctg gga acg gat atc ccc agt gaa cgt gag ata	1057
Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile	
340 345 350	
aac cgc ttg gct gct cga aac gat gaa gaa ttc cgg ttg ttt gag aag	1105
Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys	
355 360 365	
atg gat gaa gaa agg agg cta aag gag aac tac aaa tct aga ctt atg	1153
Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met	
370 375 380	
gat gga aat gag gtc cca gat tgg gtg ttt gcc aat gat aat gaa acc	1201
Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr	
385 390 395 400	
tta cgc aag aaa acc gtg gca gat gaa ttc cgg aat ata att gtt ggt	1249
Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly	
405 410 415	
tca aag aga cgt aga aag gag gtt gtc tat tcg gac tct ttt ggt gat	1297
Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp	
420 425 430	
cag tgg atg aaa tcc gac gag gga ttt gaa gag att gca aag atg act	1345
Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr	
435 440 445	
cca agg gtg aag cga act gct tat tcg cct gac att caa gtt gag tac	1393
Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr	
450 455 460	
aat gaa agg agg aaa agg ccc aag tct gtg gaa aac agc gca gat ggc	1441
Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly	
465 470 475 480	
gca agc aac cca aca cgg aca ccc gac aaa gga agg gct gga gtt tca	1489
Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser	
485 490 495	
tca tac agc aag gat gag acc gaa gat gat ggt gaa gac gaa gtc atc	1537
Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile	
500 505 510	
acc agt ggc tta cag aag ggt aac agt ttc aca tgg aag acc ctt gga	1585
Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly	
515 520 525	
aga aaa agg tca agc cac tta agt tcg tcg tcg gac tca aaa ggg cga	1633
Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg	
530 535 540	

cca tca ttc taa
Pro Ser Phe
545

1645

<210> 18
<211> 547
<212> PRT
<213> Zea mays

<220>
<221> VARIANT
<222> (0)...(0)
<223> Xaa = any amino acid

<400> 18
Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly
1 5 10 15
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe
20 25 30
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe
35 40 45
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu
50 55 60
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg
65 70 75 80
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val
85 90 95
Ile Leu Lys Cys Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln
100 105 110
Val Thr Ser Arg Glu Lys Val Ala Leu Gly Tyr Gly Ile Arg Lys Lys
115 120 125
Ala Leu Gln Asn Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro
130 135 140
Tyr Leu Phe Val Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val
145 150 155 160
Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu
165 170 175
Gln Arg Ala Gly His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu
180 185 190
Leu Asp Val Leu Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met
195 200 205
Arg Leu Asp Gly Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala
210 215 220
Asp Phe Asn Lys Lys Asn Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr
225 230 235 240
Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile
245 250 255
Ile Phe Asp Ser Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp
260 265 270
Arg Ala His Arg Ile Gly Gln Lys Asn Glu Val Arg Val Phe Val Leu
275 280 285
Val Ser Val Gly Ser Ile Glu Glu Glu Ile Leu Asp Arg Ala Lys Gln
290 295 300
Lys Met Gly Ile Asp Ala Lys Val Ile Gln Ala Gly Leu Phe Asn Thr
305 310 315 320

Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg
 325 330 335
 Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile
 340 345 350
 Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys
 355 360 365
 Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met
 370 375 380
 Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr
 385 390 395 400
 Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly
 405 410 415
 Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp
 420 425 430
 Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr
 435 440 445
 Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr
 450 455 460
 Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly
 465 470 475 480
 Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser
 485 490 495
 Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile
 500 505 510
 Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly
 515 520 525
 Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg
 530 535 540
 Pro Ser Phe
 545

<210> 19
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 19
 acaggcactc ctatccaaaa cag

23

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 20
 gaatgatggt cgcccttttg agt

23

<210> 21

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<211> 514
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6)...(514)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 21
ccnta aat ttc ttg tta ccc aaa cnt nat caa ttt cat cca gga gga ctt      50
      Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu
        1             5             10             15

ctc tca aat ggt tta ata agc cat ttg aga gtg ctt gga gat agc tcg      98
Leu Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser
          20             25             30

cct gat gaa gct tta ntg tcc gag gag gag aat ctc ttg att ata aat      146
Pro Asp Glu Ala Leu Xaa Ser Glu Glu Glu Asn Leu Leu Ile Ile Asn
          35             40             45

cgt ctg cac caa gtt ttg aga cca ttt gta ctt agg agg ctg aaa cac      194
Arg Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His
          50             55             60

aag gtt gaa aat gag ttg cct gag aag att gag aga cta ata aga tgt      242
Lys Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys
          65             70             75

gag gcc tca tca tat caa aaa ctt ttg atg aag agg gtg gaa gaa aat      290
Glu Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn
          80             85             90             95

ctt ggt tct att ggc aat tca aag gct cga tca gta cac aac tct gtc      338
Leu Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val
          100            105            110

atg gag ctt cgt aat ata tgc aat cat cca tat ctc agt cag ctt cat      386
Met Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His
          115            120            125

gca gag gag gtg gat aac ttc ata cct aaa cat tat ctg cca cca att      434
Ala Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile
          130            135            140

att aga ctt tgt ggg aag ctt gag atg ttg gac cgt tta ttg cca aaa      482
Ile Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys
          145            150            155

ttg aag gcg aca gat cat cgg gtt ctt ttc tt      514
Leu Lys Ala Thr Asp His Arg Val Leu Phe
160            165

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<210> 22
 <211> 169
 <212> PRT
 <213> Glycine max

 <220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

<400> 22
 Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu Leu
 1 5 10 15
 Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser Pro
 20 25 30
 Asp Glu Ala Leu Xaa Ser Glu Glu Asn Leu Leu Ile Ile Asn Arg
 35 40 45
 Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His Lys
 50 55 60
 Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys Glu
 65 70 75 80
 Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn Leu
 85 90 95
 Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val Met
 100 105 110
 Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His Ala
 115 120 125
 Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile Ile
 130 135 140
 Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys Leu
 145 150 155 160
 Lys Ala Thr Asp His Arg Val Leu Phe
 165

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 23
 aacccgatga tctgtcgcct tca

23

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)


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<400> 24
tcatccagga ggacttctct caa
23

<210> 25
<211> 403
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (221)...(403)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 25
tgaatatntn cttgntttta atttatgcga ntaaggattt gtgcattnngg agattagtgt 60
cnaatgaatca agtgattgnt attttatttc atgtgtcacc cagccatatt ggcagatgaa 120
atgggtcttg gcaaaacagt tcagggtacgt attctgtttt ttattatttt aatatgtttc 180
ntaatttggt tgtnttccta atcctttact tttcaagtaa gaa atg cca tat gtt 235
                                     Glu Met Pro Tyr Val
                                     1 5

ctt gtc ttc cag gcc atc aca tat tta act ttg ctg aaa cac ttg cac 283
Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu Leu Lys His Leu His
                                     10 15 20

aat gat tct ggt cca cat ctt ata gta tgt cct gct tct gtt ctg gaa 331
Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro Ala Ser Val Leu Glu
                                     25 30 35

aac tgg gaa agg gaa tta aaa agg tgg tgt cca tcc ttt tct gtt ctt 379
Asn Trp Glu Arg Glu Leu Lys Arg Trp Cys Pro Ser Phe Ser Val Leu
                                     40 45 50

caa tac cat ggg gcc gga cgt gca 403
Gln Tyr His Gly Ala Gly Arg Ala
                                     55 60

<210> 26
<211> 61
<212> PRT
<213> Glycine max

<220>
<221> VARIANT
<222> (0)...(0)
<223> Xaa = Any Amino Acid

<400> 26
Glu Met Pro Tyr Val Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu
1 5 10 15
Leu Lys His Leu His Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro

```

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Ala	Ser	Val	Leu	Glu	Asn	Trp	Glu	Arg	Glu	Leu	Lys	Arg	Trp	Cys	Pro
	35		40		45										
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50			55		60										

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 27
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<210> 28
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(25)

<400> 28
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<210> 29
 <211> 522
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)...(522)

<221> misc_feature
 <222> (0)...(0)
 <223> n = A, T, C or G

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 Val Ser Gly Arg Lys Ala Gln Tyr Ser Lys Lys Asn Ser Arg Asn Val
 1 5 10 15

gat tca ctc cct ttg atg gag ggt gaa ggg cgt gct tta aaa gtt tat 96
 Asp Ser Leu Pro Leu Met Glu Gly Glu Gly Arg Ala Leu Lys Val Tyr
 20 25 30

gga ttc aat cac gtt caa cga aca caa ttc cta cag aca ctc atg agg 144
 Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg
 35 40 45

tat ggt ttt cag aac tat gat tgg aaa gag tat ctt cct cgt ttg aag	192
Tyr Gly Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys	
50 55 60	
ggg aaa agt gtt gag gaa att cag aga tat ggt gag ctt gtc atg gcc	240
Gly Lys Ser Val Glu Glu Ile Gln Arg Tyr Gly Glu Leu Val Met Ala	
65 70 75 80	
cat ctt gta gag gac aca aat gac tca cca acc tat gca gat ggt gtg	288
His Leu Val Glu Asp Thr Asn Asp Ser Pro Thr Tyr Ala Asp Gly Val	
85 90 95	
ccg aag aaa tgc gtg ctg atg aga cat tgg tca ggc tag cca aaa tat	336
Pro Lys Lys Cys Val Leu Met Arg His Trp Ser Gly * Pro Lys Tyr	
100 105 110	
cac ttg tgg agg aga agg tgg tgc atg gag caa gga aaa tta caa aac	384
His Leu Trp Arg Arg Arg Trp Cys Met Glu Gln Gly Lys Leu Gln Asn	
115 120 125	
tct tcc cca act act tga tgt atg aat tta ctg gct tat cag gtg gaa	432
Ser Ser Pro Thr Thr * Cys Met Asn Leu Leu Ala Tyr Gln Val Glu	
130 135 140	
gaa tat gga aag ggg aac atg atc tac tgt nac tga agc ata ata agc	480
Glu Tyr Gly Lys Gly Asn Met Ile Tyr Cys Xaa * Ser Ile Ile Ser	
145 150 155	
acg ggt tgc cag tgg cat aca tat cag atn cag aga tac ggg	522
Thr Gly Cys Gln Trp His Thr Tyr Gln Xaa Gln Arg Tyr Gly	
160 165 170	

<210> 30

<211> 171

<212> PRT

<213> Oryza sativa

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Any Amino Acid

<400> 30

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20 25 30	
Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg	
35 40 45	
Tyr Gly Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys	
50 55 60	
Gly Lys Ser Val Glu Glu Ile Gln Arg Tyr Gly Glu Leu Val Met Ala	
65 70 75 80	
His Leu Val Glu Asp Thr Asn Asp Ser Pro Thr Tyr Ala Asp Gly Val	
85 90 95	

Pro Lys Lys Cys Val Leu Met Arg His Trp Ser Gly Pro Lys Tyr His
100 105 110
Leu Trp Arg Arg Arg Trp Cys Met Glu Gln Gly Lys Leu Gln Asn Ser
115 120 125
Ser Pro Thr Thr Cys Met Asn Leu Leu Ala Tyr Gln Val Glu Glu Tyr
130 135 140
Gly Lys Gly Asn Met Ile Tyr Cys Xaa Ser Ile Ile Ser Thr Gly Cys
145 150 155 160
Gln Trp His Thr Tyr Gln Xaa Gln Arg Tyr Gly
165 170

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 31
gtttctggga ggaaggctca gta 23

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 32
tatgtatgcc actggcaacc cgt 23

<210> 33
<211> 510
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (2)...(510)

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Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly
1 5 10 15

tta ata gct aca gca tgt gac gtt gat act cta atg atg aag gag cgg 97
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg
20 25 30

agc tct tta tgt gaa agt gcg gca gat gga agt tgg gtt ttg aaa tac 145
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr
35 40 45

aaa agg aaa cgg agc aag cta aca gtt agt cca tca agt gag cat gat	193
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
gct tcc tca cca ata ctg gat tct caa atg aac aat ggc tcc atc aaa	241
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
aag aag atc aaa cat gac act aac att tct cca tca acc aag aag ata	289
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
aga gga cat gac ggg tac ttc tac gag tgt gta gaa tgt gat ctc ggt	337
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
ggc aat ttg ctg tgc tgt gat agc tgt cca cga aca tac cac ttg gaa	385
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
tgt ctt aat cct cct ctc aag cgt gca cca cct gga aat tgg caa tgc	433
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	
130 135 140	
cca aga tgt cgt aca aaa aaa gtt agc ttg aag ctc tta aac aat gct	481
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala	
145 150 155 160	
gat gct gac acc tcc taa acg tga aag aa	510
Asp Ala Asp Thr Ser * Thr * Lys	
165	

<210> 34
 <211> 167
 <212> PRT
 <213> Oryza sativa

<400> 34

Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly	
1 5 10 15	
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg	
20 25 30	
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr	
35 40 45	
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	

Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys
 130 135 140
 Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala
 145 150 155 160
 Asp Ala Asp Thr Ser Thr Lys
 165

<210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1)...(23)

<400> 35
 cttacaggat ttcgggggag gtg 23

<210> 36
 <211> 23
 <212> DNA
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 <222> (1)...(23)

<400> 36
 ctttcacggt taggaggtgt cag 23

<210> 37
 <211> 667
 <212> DNA
 <213> Triticum aestivum

<220>
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 <222> (2)...(667)

<221> misc_feature
 <222> (0)...(0)
 <223> n = A, T, C, or G

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 Leu Thr Gly Thr Pro Leu Gln Asn Asn Ile Gly Glu Met Tyr Asn Leu
 1 5 10 15

ttg aac ttc cta cag cct gct tct ttc cct tct cta gca tca ttt gag 97
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu
 20 25 30

gag aag ttt aat gaa ctt gca aca gca gag aaa gtg gag gag ctg aag 145
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys
 35 40 45

aaa ctg gta gca cca cat atg ctt cga agg ctg aaa aaa gat gca atg	193
Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met	
50 55 60	
aaa aat atc ccc ccg aag aca gag cga atg gtg cct gtc gaa ctg aca	241
Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr	
65 70 75 80	
tca atc cag gct gaa tac tac cgt gct atg ctt aca aag aac tac caa	289
Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln	
85 90 95	
gta ctg cgt aat acc gga aaa ggt ggt gct cat cag tca ttg ctc aat	337
Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn	
100 105 110	
ata gta atg cag ctt cgg aaa ttt gca acc atc cat atc tta tcc tgg	385
Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp	
115 120 125	
gaa ctg aac ccg aat caa gtt cac cag att ttt gca tga aat gag aat	433
Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala * Asn Glu Asn	
130 135 140	
aaa ggc tca aca aat taa ctt tgt tgc att cta tgc tca aag tgt tac	481
Lys Gly Ser Thr Asn * Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr	
145 150 155	
aca gtg atg ggc atc gtg ttc taa ttt tcc aga tga cta aac tct tga	529
Thr Val Met Gly Ile Val Phe * Phe Ser Arg * Leu Asn Ser *	
160 165 170	
cat ccc gaa gat anc gac ccg gaa ttg gca taa aca ntn aaa gag naa	577
His Pro Glu Asp Xaa Asp Pro Glu Leu Ala * Thr Xaa Lys Glu Xaa	
175 180 185	
tgg tcg tgt cgt ggg tga cnc aag cac ata nct tca aca gaa ana cgt	625
Trp Ser Cys Arg Gly * Xaa Lys His Ile Xaa Ser Thr Glu Xaa Arg	
190 195 200	
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Leu Ile Cys Thr Thr Ala Cys Xaa Tyr * Xaa Xaa Val Xaa	
205 210	

<210> 38
 <211> 214
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

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 20 25 30
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys
 35 40 45
 Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met
 50 55 60
 Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr
 65 70 75 80
 Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln
 85 90 95
 Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn
 100 105 110
 Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp
 115 120 125
 Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala Asn Glu Asn Lys
 130 135 140
 Gly Ser Thr Asn Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr Thr Val
 145 150 155 160
 Met Gly Ile Val Phe Phe Ser Arg Leu Asn Ser His Pro Glu Asp Xaa
 165 170 175
 Asp Pro Glu Leu Ala Thr Xaa Lys Glu Xaa Trp Ser Cys Arg Gly Xaa
 180 185 190
 Lys His Ile Xaa Ser Thr Glu Xaa Arg Leu Ile Cys Thr Thr Ala Cys
 195 200 205
 Xaa Tyr Xaa Xaa Val Xaa
 210

<210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222> (1)...(23)

<400> 39
 gttgactgga accccattac aga

23

<210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

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 <222> (1)...(23)

<400> 40
 catgccgttg tacaaatcaa acg

23

<210> 41
 <211> 12561

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (1)...(12561)

<223> Zmpk1 genomic sequence

<221> misc_feature

<222> (0)...(0)

<223> n = A, T, C, or G

<400> 41

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tgcaagctat	ggcaagagct	catcgcttag	gacagactag	taaggatttt	taccttacac	180
tttatattgt	ataaaaaaac	agattttcaa	taagttttgt	ggtgatttta	taattttcat	240
ctgtttttct	tttaggtgat	gatatacagg	cttgtagacc	gaggtacaat	tgaggagcga	300
atgatgcagc	ttacaaaaaa	gaagatttta	ttggagcact	tagttgttgg	tcgactcacc	360
aaagctaata	atgtcaatca	ggtatgttga	ctacttttta	atgggtgaatt	ttgtaaacca	420
tcaacttagg	ttgatctttt	atggcctaag	ctattttatga	attcattttat	ggattgaggg	480
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aaactaacgg	gtgacaaata	ttcgagaacg	gaggtagtac	tagtaccttc	tgtctgggat	600
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Arg	Phe	Asp	Val	Leu	Leu	Thr	Ser	Tyr	Glu	Met	Ile	Asn	Met	Asp	Ser	
			405						410					415		
Ser	Ile	Leu	Lys	Asn	Ile	Glu	Trp	Glu	Cys	Leu	Val	Val	Asp	Glu	Gly	
			420					425					430			
His	Arg	Leu	Lys	Asn	Lys	Asp	Ser	Lys	Leu	Phe	Gly	Gln	Leu	Lys	Asp	
		435					440					445				
Tyr	Asn	Thr	Lys	His	Arg	Val	Leu	Leu	Thr	Gly	Thr	Pro	Val	Gln	Asn	
	450					455					460					
Asn	Leu	Asp	Glu	Leu	Phe	Met	Leu	Met	His	Phe	Leu	Glu	Gly	Glu	Ser	
465					470					475						

				565				570				575				
His	Gly	Phe	Met	Ile	Asp	Glu	Pro	Asp	Leu	Glu	Pro	Ala	Asn	Pro	Glu	
				580					585					590		
Glu	Gly	Leu	Arg	Arg	Leu	Leu	Asp	Ser	Ser	Gly	Lys	Met	Gln	Leu	Leu	
				595					600					605		
Asp	Lys	Met	Met	Val	Lys	Leu	Lys	Glu	Gln	Gly	His	Arg	Val	Leu	Ile	
				610					615					620		
Tyr	Ser	Gln	Phe	Gln	His	Met	Leu	Asp	Leu	Leu	Glu	Asp	Tyr	Leu	Ser	
				625					630					635		
Tyr	Arg	Lys	Trp	Thr	Tyr	Glu	Arg	Ile	Asp	Gly	Lys	Ile	Ser	Gly	Ala	
				645					650					655		
Asp	Arg	Gln	Ile	Arg	Ile	Asp	Arg	Phe	Asn	Ala	Lys	Asn	Ser	Thr	Arg	
				660					665					670		
Phe	Cys	Phe	Leu	Leu	Ser	Thr	Arg	Ala	Gly	Gly	Leu	Gly	Ile	Asn	Leu	
				675					680					685		
Ala	Thr	Ala	Asp	Thr	Val	Ile	Ile	Tyr	Asp	Ser	Asp	Trp	Asn	Pro	His	
				690					695					700		
Ala	Asp	Leu	Gln	Ala	Met	Ala	Arg	Ala	His	Arg	Leu	Gly	Gln	Thr	Ser	
				705					710					715		
Lys	Val	Met	Ile	Tyr	Arg	Leu	Val	Ser	Arg	Gly	Thr	Ile	Glu	Glu	Arg	
				725					730					735		
Met	Met	Gln	Leu	Thr	Lys	Lys	Lys	Ile	Leu	Leu	Glu	His	Leu	Val	Val	
				740					745					750		
Gly	Arg	Leu	Thr	Lys	Ala	Asn	Asn	Val	Asn	Gln	Glu	Glu	Leu	Asp	Asp	
				755					760					765		
Ile	Ile	Arg	Tyr	Gly	Ser	Lys	Glu	Leu	Phe	Glu	Asp	Glu	Asn	Asp	Glu	
				770					775					780		
Ser	Arg	Gln	Ile	His	Tyr	Asp	Glu	Ala	Ala	Ile	Glu	Arg	Leu	Leu	Asp	
				785					790					795		
Arg	Asp	Gln	Val	Asp	Gly	Asp	Glu	Ser	Val	Glu	Asp	Glu	Glu	Glu	Asp	
				805					810					815		
Gly	Phe	Leu	Lys	Gly	Phe	Lys	Val	Ala	Asn	Phe	Glu	Tyr	Ile	Asp	Glu	
				820					825					830		
Ala	Lys	Ala	Gln	Ala	Glu	Lys	Glu	Glu	Ala	Arg	Arg	Lys	Ala	Ala	Ala	
				835					840					845		
Glu	Ala	Glu	Asn	Ser	Glu	Arg	Asn	Tyr	Trp	Asp	Glu	Leu	Leu	Lys	Asp	
				850					855					860		
Arg	Tyr	Asp	Val	Gln	Lys	Val	Glu	Glu	His	Thr	Ala	Met	Gly	Lys	Gly	
				865					870					875		
Lys	Arg	Ser	Arg	Lys	Gln	Met	Ala	Ala	Ala	Asp	Glu	Asp	Asp	Ile	His	
				885					890					895		
Asp	Leu	Ser	Ser	Glu	Asp	Glu	Asp	Tyr	Ser	Leu	Glu	Asp	Asp	Ile	Ser	
				900					905					910		
Asp	Asn	Asp	Thr	Ser	Leu	Gln	Gly	Asn	Ile	Ser	Gly	Lys	Arg	Gly	Gln	
				915					920					925		
Tyr	Ser	Lys	Arg	Lys	Ser	Arg	Asn	Val	Asp	Ser	Ile	Pro	Leu	Met	Glu	
				930					935					940		
Gly	Glu	Gly	Arg	Thr	Leu	Arg	Val	Leu	Gly	Phe	Asn	His	Ala	Gln	Arg	
				945					950					955		
Ala	Met	Phe	Leu	Gln	Thr	Leu	Asn	Arg	Phe	Gly	Phe	Gln	Asn	Tyr	Asp	
				965					970					975		
Trp	Lys	Glu														

1010 1015 1020
 Asp Asp Val Leu Val Arg Ile Ala Asn Ile Ser Leu Ile Glu Glu Lys
 1025 1030 1035 1040
 Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn Ile Phe Pro Asn Tyr
 1045 1050 1055
 Leu Leu Tyr Glu Phe Gln Gly Leu Ser Gly Gly Arg Ile Trp Lys Ala
 1060 1065 1070
 Glu His Asp Leu Leu Leu Leu Arg Gly Ile Leu Lys His Gly Tyr Ala
 1075 1080 1085
 Arg Trp Gln Tyr Ile Ser Asp Asp Arg Glu Asn Gly Leu Phe Glu Ala
 1090 1095 1100
 Ala Arg Arg Glu Leu His Leu Pro Ser Val Asn Glu Ile Ile Gly Ala
 1105 1110 1115 1120
 Gln Leu Asn Glu Ala Asn Gly Asn Leu Glu Gly Ala Gln Glu Gly Gln
 1125 1130 1135
 Ala Asn Thr Thr Ser Met Ser His Tyr Lys Glu Ile Gln Arg Lys Ile
 1140 1145 1150
 Val Glu Phe Leu Arg Lys Arg Tyr His Leu Met Glu Arg Ala Leu Asn
 1155 1160 1165
 Leu Glu Tyr Ala Val Ile Lys Lys Lys Ile Pro Val Pro Asp Asp Ile
 1170 1175 1180
 Thr Glu Gln Gly Val Pro Ala Gly His Ala Pro Leu Ile Pro Asp Ile
 1185 1190 1195 1200
 Ser Glu Leu Leu Arg Glu Leu Pro Asn Leu Glu Pro Ile Ser Thr Asn
 1205 1210 1215
 Glu Leu Ile Ser Glu Gly Thr Ala Gly Gln Leu Gln Val Pro His Leu
 1220 1225 1230
 Tyr Asn Lys Met Cys Gly Val Leu Glu Glu Ser Gly Ala Tyr Ala Leu
 1235 1240 1245
 Ser Ser Phe Phe Gly Asp Lys Ser Ala Ser Ser Thr Leu Ala Asn Ser
 1250 1255 1260
 Leu Arg Gln Phe Glu Thr Val Cys Glu Asn Val Val Glu Ala Leu Arg
 1265 1270 1275 1280
 Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys Glu Glu Leu Val Asp
 1285 1290 1295
 Ala Ala Thr Lys Ala Ala Ala Ala Ala Pro Gln Gln Asp Ser Gly
 1300 1305 1310
 His Asp Ala Pro His Gly Gln Ser Ser Thr Ala Lys Ala Asp Met Glu
 1315 1320 1325
 Ile Asp Gly Phe Val Gly Ser Arg Val Ala Arg Lys Gly Ile Pro Ser
 1330 1335 1340
 Asn His Tyr Val Tyr Cys Gly Gln Asn Val Arg Tyr Ile Leu
 1345 1350 1355